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1	15 16	30 31	45 46	60 61	75 76	90
1 mtblder	MNEI.VDTTTEHYLRTI	YOLEEGVTPLRARI	AERLDQSGPTVSQTV	SRNERDGLLRVAGDR	HLELTEKGRALAIIV	MRKHRLAERLLVDVI
2 dtxr	MKOLVDTTTEHYLRTI	YELEEGVTPLRARI	AERLEQSGPTVSQTV	AMNERDGLVVASD-	SLQMTPTGRTLATAV	MRKHRLAERLLTDII
3 staphepislr	-----MTVSCPPPS--T	SEREQ-----ARAL	CLRLLTARSRTRAEL	AGQLAKRGYPEDIGN	RVLORLAAGLVDDT	65
1	105 106	120 121	135 136	150 151	165 166	180
1 mtblder	GLPWEEVHAEACRWE	HVMSDEVERRLVKVL	NNPTTSPFGNPIPL	VELGVGPEPGADDAN	LVRLTLPAGSPVAV	VVRQLTEHVQGDIDL
2 dtxr	GLDINKVHDEACRWE	HVMSDEVERRLVKVK	DVSR-SPEGNPIPL	DELGVGNS--DAAAP	GTRVIDAATSMRKKV	RIVQINEIFQVETDQ
3 staphepislr	DFAEQWVQSRANAA	KSKRALAEELIAKGV	DDDVITTVLGGIDAG	AERGRAEK--LVRAR	LRREVLIDDGTDEAR	VSRRLVAMLAARRG-Y
181	195 196	210 211	225 226	240 241	255 256	270
1 mtblder	ITRLKDAGVVPNARV	TVETTPGGGVTVIIP	GHEVTLPHIEMAHAV	KVEKV	230	
2 dtxr	FQLLDADIRVGSEVE	IVDRD--GHITLSHN	GKD-VELLDDLAITI	RIEEL	223	
3 staphepislr	GOTLACEVVIAELAA	ERERR--RV-----	-----	-----	174	

FIGURE 1

1	15	16	30	31	45	46	60	61	75	76	90	85
1 M1.	MNDLVDTTEYLRTI	YDLEEEGIVTPLRAR	IAER-----	PTVSQT	VSMEKDCILRVAGN	RHLELTGGRAMAIA	VMRKHRLAERLLVDV					85
2 TB	MNELVDTEYLRTI	YDLEEEG-VTPLRAR	IAERLDOSGPTVSQT	VSMEKDCILRVAGD	RHLELTGGRAMAIA	VMRKHRLAERLLVDV						89
3 M3	MNDLVDTTEYLRTI	YDLEEEG-VVPLRAR	IAERLDOSGPTVSQT	VSMEKDCILRVAGD	RHLELTGGRAMAIA	VMRKHRLAERLLVDV						89
4 M4b	MTVSCPPSTSER---	EEQARALCLRL	TARS-----	RTNREL	AGQLAKGYPEDIGN	RVLID-----	RLAAGV	LYDITDFAEQ-----				70
1	91	105	106	120	121	135	136	150	151	165	166	180
1 M1.	IGLPMEEVHAEACRM	EHVMSDEVERRLIKV	LNPPTSPFGNPIRG	LLDLGAGPDASANA	KLVRLTELPSGSPVA	VVRQLTEHVD-DID						174
2 TB	IGLPMEEVHAEACRM	EHVMSDEVERRLIKV	LNPPTSPFGNPIRG	LLDLGAGPDASANA	KLVRLTELPSGSPVA	VVRQLTEHVD-DID						179
3 M3	IGLPMEEVHAEACRM	EHVMSDEVERRLIKV	LNPPTSPFGNPIRG	LLDLGAGPDASANA	KLVRLTELPSGSPVA	VVRQLTEHVD-DID						179
4 M4b	----WQGS-RRANAA	KSRRALAEELHAKGV	DDDVITTVLGG-IDA	GAERGR--AEKLVRA	RLRREVLIDDTDEA	RVSRLVAMLA----						148
1	181	195	196	210	211	225	226	240	241	255	256	270
1 M1.	LITRLKDTGVVPPNAR	VTVETSPAGNVITII	PGHENVTLPHEMANA	VKVEKV----				225				225
2 TB	LITRLKDTGVVPPNAR	VTVETSPAGNVITII	PGHENVTLPHEMANA	VKVEKV----				230				230
3 M3	LITRLKDTGVVPPNAR	VTVETSPAGNVITII	PGHENVTLPHEMANA	VKVEKV----				233				233
4 M4b	---RQYQOTLACEV	VIAELAEERERRRV-	-----	-----	-----	-----	-----	174				174

FIGURE 2

1	10	20	30	40	50	60	
B1 DtxR		MKDLVDTTEM	YLRTIYELEE	EGIVPLRARI	AERLEQSGPT	VSQTVARMER	DGLVHVSPDR
Cd DtxR		MKDLVDTTEM	YLRTIYELEE	EGVTPLRARI	AERLEQSGPT	VSQTVARMER	DGLVVVASDR
Mt IdeR		MNELVDTTEM	YLRTIYDLEE	EGVTPLRARI	AERLDQSGPT	VSQTVSRMER	DGLLRVAGDR
Ms IdeR		MNDLVDTTEM	YLRTIYDLEE	EGVVPRLARI	AERLDQSGPT	VSQTVSRMER	DGLLRVAGDR
M1 IdeR		MNDLVDTTEM	YLRTIYDLEE	EGIVTPLRARI	AER PT	VSQTVSRMER	DGLLRVAGNR
S1 DesR		MSGLIDTTEM	YLRTILELEE	EGVVPMRARI	AERLDQSGPT	VSQTVARMER	DGLVSVAAADR
Se SirR	M	LTEEKED	YLKAILTNDG	DVSFVSNKKL	SQFLNIKPPS	VSEMVGRLK	EGYVETKHYK
Sa SirR	M	LTEEKED	YLKAILTNNG	DNFVTNKIL	SQFLNIKPPS	VSEMVGRLK	AGYVETKPYK
Ef	M	TPNRED	YKLIFELGG	DEVKVNKKQI	VSGLDVSAAS	VSEMISKLVK	EDLVEHSPYQ
Sg	M	TPNKED	YLKCLYELGT	RHNKITNKEI	AGLMQVSPPA	VTEMMKKLLA	EELLIKDKKA
Sm	M	TPNKED	YLKIIYELSE	RDEKISNKQI	AEKMSVSAPA	VSEMVKKLLL	EDLVKDKQA
Spn	M	TPNKED	YLKCIYEIGI	DLHKITNKEI	AARMQVSPPA	VTEMIKRMKS	ENLILKDKEC
Spy	M	TPNKED	YLKCIYEIGI	DLHKITNKEI	AARMQVSPPA	VTEMIKRMKS	ENLILKDKEC
CONSENSUS		M--*-----E*	YL*-I*-----	-----NK--*	*-----P-	*****-----*	*-L-----
		70	80	90	100	110	120
B1 DtxR		SLEMTPEGRS	LAIAMVRNDR	LAERLLTDII	GLDIHKVHDE	ACRWEHVMSD	EVERRLVEVL
Cd DtxR		SLQMTPTGRT	LATAVMRKHR	LAERLLTDII	GLDINKVHDE	ACRWEHVMSD	EVERRLVKVL
Mt IdeR		HLELTEKGRA	LAIAMVRKHR	LAERLLVDVI	GLPWEEVHAE	ACRWEHVMSE	DVERRLVKVL
Ms IdeR		HLELTDKGRA	LAVAVMRKHR	LAERLLVDVI	LPWEDGVHAE	ACRWEHVMSE	EVERRLVQVL
M1 IdeR		HLELTTKGRA	MAIAMVRKHR	LAERLLVDVI	GLPWEEVHAE	ACRWEHVMSE	DVERRLIKVL
S1 DesR		HLELTDGRR	LATVRMRKHR	LAECLLVDVI	GLEWEQVHAE	ACRWEHVMSE	AVERRVLELL
Se SirR		GARLTEEGLK	QTLDIKRHR	LLRLFLIEIL	QYNWEEVHOE	AEILEHRISD	LFVERLDKIL
Sa SirR		GVRLTEDGLT	HTLDII RHR	LLEFLIEIL	KYNWEEVHOE	AEILEHRISD	LFVERLDSLL
Ef		GVQLTEKGLK	KASTLIRKHR	IWEVFLVEHL	NYTWNDVHEE	AEVLEHVTSTQ	TLVNRLADYL
Sg		GYLLTDLGLK	LVSDLYRKHR	LIEVFLVHHL	GYTTEEIHEE	AEVLEHTVSD	HFVERLDQLL
Sm		GYLLTKKGQI	LASSLYRKHR	LIEVFLMNLH	NYTADEIHEE	AEVLEHTVSD	VFVERLDKFL
Spn		GYLLTDLGLK	LVSELYRKHR	LIEVFLVHHL	DYTSQIHEE	AEVLEHTVSD	LFVERLDKLL
Spy		GYLLTDLGLK	LVSELYRKHR	LIEVFLVHHL	DYTSQIHEE	AEVLEHTVSD	LFVERLDKLL
CONSENSUS		---LT-G--	-----**HR	L--**L---L	-----H-E	A*-EH-S*	***R***-L
		130	140	150	160	170	180
B1 DtxR		DDVHRSPPGN	PIPGLEIGL	DQADEPDSGV	RAIDLPLGEN	LKARIVQLNE	ILQVDLEQFQ
Cd DtxR		KDVSRSPPGN	PIPGLELGV	GNSDAAAPGT	RVIDAATSMP	RKVRIVQINE	IFQVETDQFT
Mt IdeR		NNPTTSPFGN	PIPGLEVELV	GPEPGADDAN	LVRLTELPAG	SPVAVVVRL	TEHVQGDIDL
Ms IdeR		ENPTTSPFGN	PIPGLELAV	TPGVNTEDVS	LVRLTELPVG	MPVAVVVRL	TEHVQGDIDL
M1 IdeR		NNPTTSPFGN	PIPGLDLGA	GPDSAAANAK	LVRLTELPAG	SPVAVVVRL	TEHV DDIDL
S1 DesR		RHPTESPYGN	PIPGLEELGE	TDGADPFLDE	GMVSLADLDP	GQEGKTVVVR	RIGEPIDTDA
Se SirR		NFPKTCPHGG	VIP	R GNSDAAAPGT	SILNFEPGER	VTVRRV RDK	TELL
Sa SirR		NFPETCPHGG	VIP	R NNEYKEYIT	TILNYEPGDI	VTIKRV RDK	TDLL
Ef		NHPEFCPHGG	VIPEDNQPIH	EEKRQTLTDY	PVGTKIRIAR	VLDEKELLDY	LVSIDLNIQE
Sg		DYPKACPHGG	TIPAKGELLV	EKHKLTLLEA	KEKGDYILAR	VHDNFDLLTY	LERNGLQVGK
Sm		NYPKVCPHGG	TIPGHGQPLV	ERYRTTLKGV	TEMGVYLLKR	VQDNFQLLKY	MEQHHLKIGD
Spn		GFPKTCPHGG	TIPAKGELLV	EINNPLADI	KEAGAYRLTR	VHDSFDILHY	LDKHSIHIGD
Spy		GFPKTCPHGG	TIPAKGELLV	EINNPLADI	KEAGAYRLTR	VHDSFDILHY	LDKHSIHIGD
CONSENSUS		--P--*P*G*	-IP-***--	-----	-----	-----	-----

FIGURE 3

	190	200	210	220	230
B1 DtxR	ALTDAGVEIG	TEVDIINEQG	RVVITHNGSS	VELIDDLAHA	VRVEKVEG
Cd DtxR	QLLDADIRVG	SEVEIVDRDG	HITLSHNGKD	VELLDDLAHT	IRIEEL
Mt IdeR	ITRLKDAGVV	PNARVTVETT	PGGGVTIVIP	GHENVTLPHE	MAHAVKVEKV
Ms IdeR	IGRLKEAGVV	PNARVTVEAN	NNGGVMIVIP	GHEQVELPHH	MAHAVKKKVE KVEKV
M1 IdeR	ITRLKDTGVV	PNARVTVETS	PAGNVIIIIP	GHENVTLPHE	MAHAVKVEKV

S1 DesR	QLMYTLRRAG	VQPGSVSVST	ESAGGVLVGS	GGEAAELEAD	TASHVFAKR
Sa SirR	VYLSSKDIYI	GNTVEIVSKD	DTNKVIILKR	NDIVTILSYE	NAMNIFAEK
Sa SirR	IYLSSKDISI	GNEVEIVSKD	EMNKVIIIKR	NDNVIIIVSYE	NAMNMFAEK
Ef	EYTIKEIAAY	EGPITIYNEN	KELSVSFKAA	NTIFVEPLIR	ESEEN
Sg SgoR	TIRFLGYDDF	SHLYSLEVDG	QEIQLAQPIA	QOIYVEKI	
Sm SloR	ELRLLEYDAF	AGAYTIEKDG	EQLQVTSAVA	SQIYIEKKAY	
Spn	QLQVKQFDGF	SNTFTILSND	EDLQVNMDIA	KOLYVEKIN	
Spy	QLQVKQFDGF	SNTFTILSND	EDLQVNMDIA	KOLYVEKIN	

CONSENSUS -----

FIGURE 3 cont.

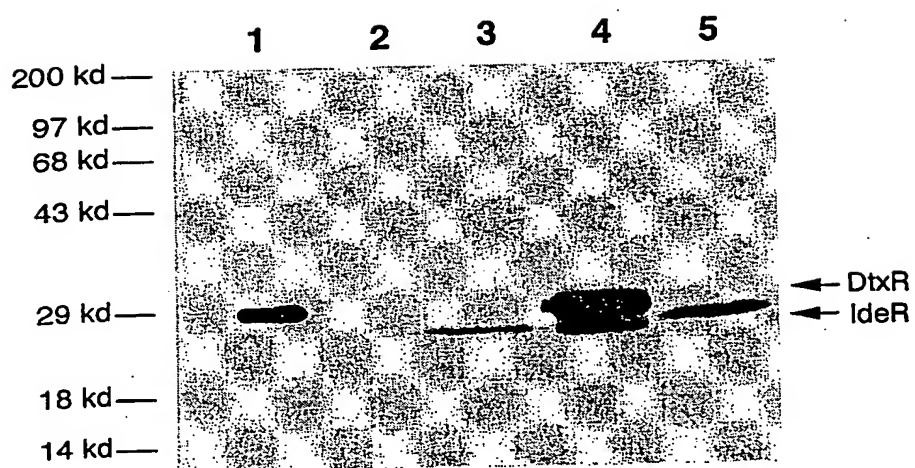


FIGURE 4

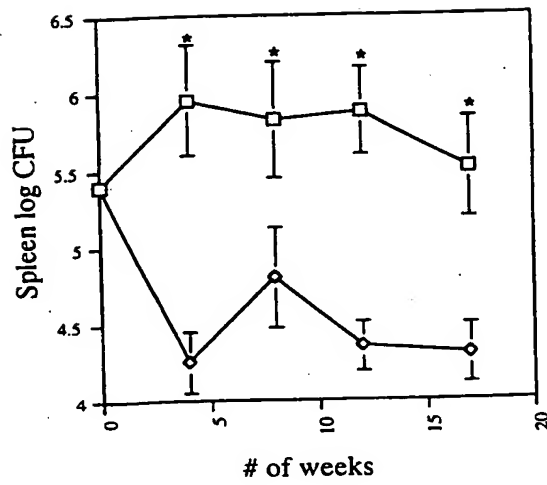


FIGURE 5A

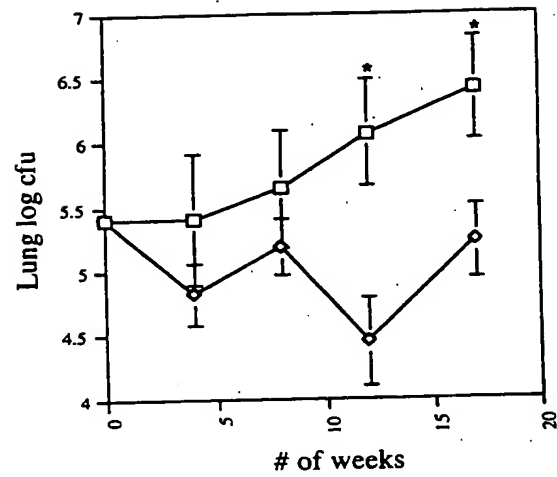


FIGURE 5B

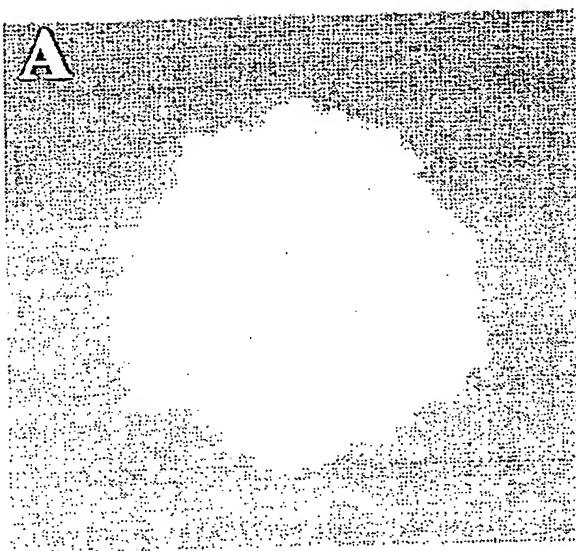


FIGURE 6A

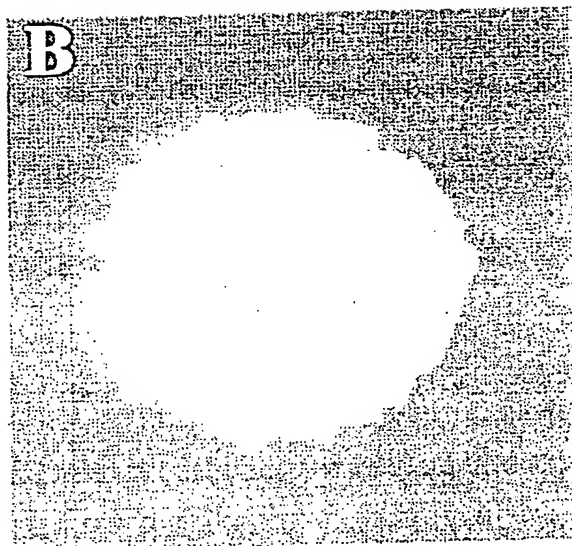


FIGURE 6B

G T A G G T T A G G C T - A A C C T A T																				Consensus Sequence
T	T	A	G	G	T	T	A	G	G	C	T	-	A	A	C	C	T	A	A	Published Consensus
T	T	A	G	G	A	T	A	G	C	T	T	-	T	A	C	C	T	A	A	<i>tox</i> PO <i>C.diphtheriae</i>
T	T	A	G	G	T	T	A	G	G	C	T	-	C	A	C	C	T	A	A	<i>desA</i> PO <i>S.pilosus</i>
C	C	A	G	G	G	T	A	T	C	T	A	-	A	T	C	C	T	G	T	16S ribosomal RNA
G	C	A	G	G	C	C	A	G	T	G	A	-	A	A	C	C	T	G	T	19 kDa antigen
A	C	A	G	G	T	G	G	T	G	C	T	C	A	A	C	C	A	C	G	<i>htrA</i> homologue
G	A	A	G	G	T	A	A	C	G	T	T	C	A	A	C	C	A	A	T	<i>phoP</i> homologue
G	C	A	G	G	T	G	A	C	C	G	T	C	A	A	C	C	G	A	T	<i>adhB</i> homologue
G	A	A	G	G	T	C	A	A	C	C	A	-	A	A	C	A	A	G	A	<i>narG</i> homologue

FIGURE 7

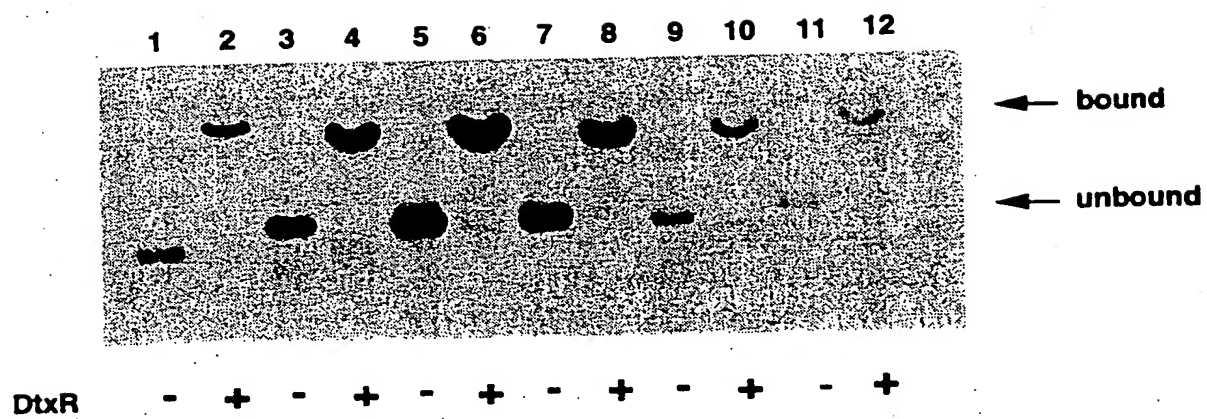


FIGURE 8

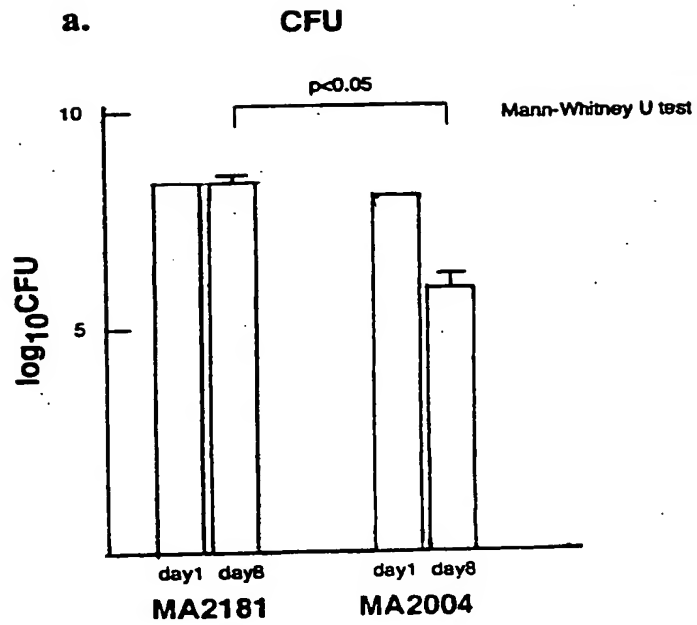


FIGURE 9A

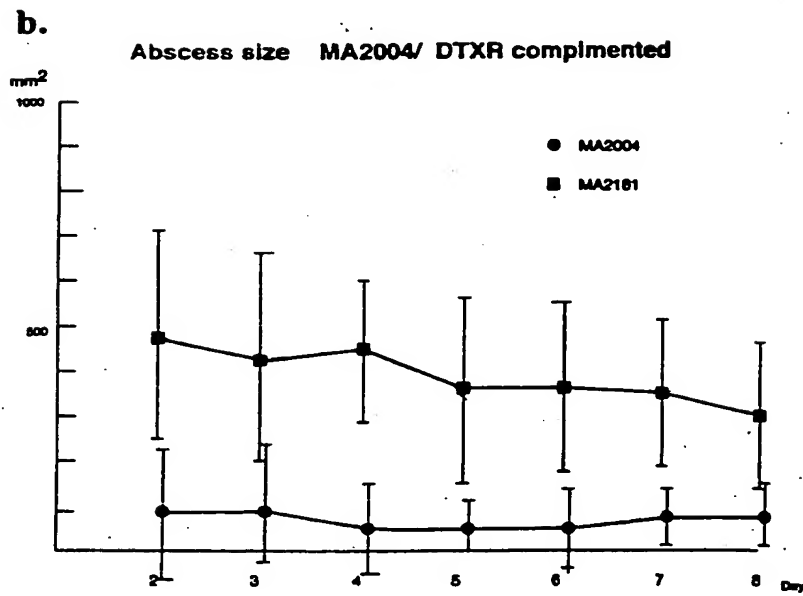


FIGURE 9B